

↓ is the regions for β-sheet deletions

*: is the N-linked glycosylation sites for subtype C TV1 and TV2. Possible mutation (N→ Q) or deletions can be performed.

	1	50
SF162	(1) ----MDAMKRGLCVLLLCGSAVFVSPSAVEK	TV1.8_2
TV1.8_2	(1) MRVMGTQKNCQQQWIIWGLGFWMLMICNTED	TV1.8_5
TV1.8_5	(1) MRVMGTQKNCQQQWIIWGLGFWMLMICNTED	TV2.12.5/1
TV2.12.5/1	(1) MPARGILKNYRHHWWIIGLIGFWMLMCMCNVKG	Consensus
Consensus	(1) MRVMGTQKNCQQQWIIWGLIGFWMLMICNVBDLWVT	

	51	100
SF162	(47) FCASDAKAYETEVHNVWATHACVTPDPNPQEI	TV1.8_2
TV1.8_2	(51) FCASDAKAYETEVHNVWATHACVTPDPNPQEI	TV1.8_5
TV1.8_5	(51) FCASDAKAYETEVHNVWATHACVTPDPNPQEI	TV2.12.5/1
TV2.12.5/1	(51) FCASDAKAYETEVHNVWATHACVTPDPNPQEI	Consensus
Consensus	(51) FCASDAKAYETEVHNVWATHACVTPDPNPQEI	

	101	↓	150
SF162	(97) QMHEDIISLWDQSLKPCVKLTPLCVTLNCTNT	TV1.8_2	
TV1.8_2	(101) QMHEDIISLWDQSLKPCVKLTPLCVTLNCTNT	TV1.8_5	
TV1.8_5	(101) QMHEDIISLWDQSLKPCVKLTPLCVTLNCTNT	TV2.12.5/1	
TV2.12.5/1	(101) QMHEDIISLWDQSLKPCVKLTPLCVTLNCTNT	Consensus	
Consensus	(101) QMHEDIISLWDQSLKPCVKLTPLCVTLNCTNT		

	151	200
SF162	(139) WKEMDRGEIHKCSKATTSISINEMKQYALF	TV1.8_2
TV1.8_2	(151) TGIYNIEEMKCSKATTSISINEMKQYALF	TV1.8_5
TV1.8_5	(151) NATYKYEEMKCSKATTSISINEMKQYALF	TV2.12.5/1
TV2.12.5/1	(141) -----KEMKCSKATTSISINEMKQYALF	Consensus
Consensus	(151) A Y EEMKCSKATTSISINEMKQYALF	

	201	↓	250
SF162	(185) RLINCNSTITQACPKVSFDPPIPHYCAPAGY	TV1.8_2	
TV1.8_2	(199) RLINCNSTITQACPKVSFDPPIPHYCAPAGY	TV1.8_5	
TV1.8_5	(199) RLINCNSTITQACPKVSFDPPIPHYCAPAGY	TV2.12.5/1	
TV2.12.5/1	(185) RLINCNSTITQACPKVSFDPPIPHYCAPAGY	Consensus	
Consensus	(201) RLINCNSTITQACPKVSFDPPIPHYCAPAGY		

	251	300
SF162	(235) VETVQCTHGIRKPVVSTQQLLNGSLABEGII	TV1.8_2
TV1.8_2	(249) VETVQCTHGIRKPVVSTQQLLNGSLABEGII	TV1.8_5
TV1.8_5	(249) VETVQCTHGIRKPVVSTQQLLNGSLABEGII	TV2.12.5/1
TV2.12.5/1	(235) VETVQCTHGIRKPVVSTQQLLNGSLABEGII	Consensus
Consensus	(251) VETVQCTHGIRKPVVSTQQLLNGSLABEGII	

	301*	350
SF162	(285) VEINCTRPNNNTRKSVRIGPGQAPYATNDI	TV1.8_2
TV1.8_2	(299) VEINCTRPNNNTRKSVRIGPGQAPYATNDI	TV1.8_5
TV1.8_5	(299) VEINCTRPNNNTRKSVRIGPGQAPYATNDI	TV2.12.5/1
TV2.12.5/1	(285) VEINCTRPNNNTRKSVRIGPGQAPYATNDI	Consensus
Consensus	(301) VEINCTRPNNNTRKSVRIGPGQAPYATNDI	

FIGURE 105A

	351	*		*	400
SF162	(335)	KQIVTKLQAQFGNKT-IVFKQS	↓	β20/β21	↓
TV1.8_2	(349)	QQVMKKLGEHFPNKT-IQFKPHAGDLHITMSEFNCBSPFYCTHNLN			
TV1.8_5	(349)	QQVMKKLGEHFPNKT-IKFPHPAGDLHITMSEFNCBSPFYCTHNLN			
TV2.12-5/1	(335)	QRVSQKLQELFPHNSTGIKFAFHGGDLKITTTSSINCGRFFPYCTHNLN			
Consensus	(351)	QQVMKKLGEHFPNKT IKFKPHAGDLHITMSEFNCBSPFYCTHNLN			
	401	*	*		450
SF162	(384)	STWNN-----TIGPN-NTNGT	↓	β20/β21	↓
TV1.8_2	(398)	STYHS---NNGTYKYNGNSSSP			
TV1.8_5	(398)	STYTP---KNGTYKYNGNSSLP			
TV2.12-5/1	(385)	STVSGTCTNGTCMSN--NTER			
Consensus	(401)	STYHN NGTYKYNGNSS PITLQCKIKQIIRMWQGVQAMYPPIAG			
	*				
	451	*	*	*	500
SF162	(427)	QIRCSSNITGLLLTRDGGKEISNT--TETFRPGGDMRDNRRSELYKYK			
TV1.8_2	(445)	NITCRSNITGLLLTRDGGFNNTTNN--TETFRPGGDMRDNRRSELYKYK			
TV1.8_5	(445)	NITCRSNITGLLLTRDGGFNNTTNDTETFRPGGDMRDNRRSELYKYK			
TV2.12-5/1	(433)	NITCRSNITGLLLTRDGGFNNTTET--TETFRPGGDMRDNRRSELYKYK			
Consensus	(451)	NITCRSNITGLLLTRDGGFNNTTNT TETFRPGGDMRDNRRSELYKYK			
	501				550
SF162	(475)	VEIKPLGIAPTAKKRRVQREKRAVGIGAVPLGFLGAAGSTMGAASTITLT			
TV1.8_2	(493)	VEIKPLGIAPTAKKRRVQREKRAVGIGAVPLGFLGAAGSTMGAASTITLT			
TV1.8_5	(495)	VEIKPLGIAPTAKKRRVQREKRAVGIGAVPLGFLGAAGSTMGAASTITLT			
TV2.12-5/1	(480)	VEIKPLGIAPTAKKRRVQREKRAVGIGAVPLGFLGAAGSTMGAASTITLT			
Consensus	(501)	VEIKPLGIAPTAKKRRVQREKRAVGIGAVPLGFLGAAGSTMGAASTITLT			
	551				600
SF162	(525)	VQARQLLSGIVQQSNLLKAEAQQHMLQLTVWGIKQLQARVLAITERLYK			
TV1.8_2	(543)	VQARQLLSGIVQQSNLLKAEAQQHMLQLTVWGIKQLQARVLAITERLYK			
TV1.8_5	(545)	VQARQLLSGIVQQSNLLKAEAQQHMLQLTVWGIKQLQARVLAITERLYK			
TV2.12-5/1	(530)	VQARQLLSGIVQQSNLLKAEAQQHMLQLTVWGIKQLQARVLAITERLYK			
Consensus	(551)	VQARQLLSGIVQQSNLLKAEAQQHMLQLTVWGIKQLQARVLAITERLYK			
	601	*	*	*	650
SF162	(575)	DQQLLGIVGCSGKLICTTAVPWNSSSNKSEADWDNMTWQWDRDISNY			
TV1.8_2	(593)	DQQLLGIVGCSGKLICTTAVPWNSSSNKSEADWDNMTWQWDRDISNY			
TV1.8_5	(595)	DQQLLGIVGCSGKLICTTAVPWNSSSNKSEADWDNMTWQWDRDISNY			
TV2.12-5/1	(580)	DQQLLGIVGCSGKLICTTAVPWNSSSNKSEADWDNMTWQWDRDISNY			
Consensus	(601)	DQQLLGIVGCSGKLICTTAVPWNSSSNKSEADWDNMTWQWDRDISNY			
	651				700
SF162	(625)	NTIYRLLEDSONQQEKNEKDLLELDKWNLNWNPDISNWLWYIKIFIMI			
TV1.8_2	(643)	NTIYRLLEDSONQQEKNEKDLLELDKWNLNWNPDISNWLWYIKIFIMI			
TV1.8_5	(645)	NTIYRLLEDSONQQEKNEKDLLELDKWNLNWNPDISNWLWYIKIFIMI			
TV2.12-5/1	(630)	NTIYRLLEDSONQQEKNEKDLLELDKWNLNWNPDISNWLWYIKIFIMI			
Consensus	(651)	NTIYRLLEDSONQQEKNEKDLLELDKWNLNWNPDISNWLWYIKIFIMI			
	701				750
SF162	(675)	VGGLIGLRIIFAVLSIVNRVQGYSPFSQTLTPSPRGFDRLGGIEEGG			
TV1.8_2	(693)	VGGLIGLRIIFAVLSIVNRVQGYSPFSQTLTPSPRGFDRLGGIEEGG			
TV1.8_5	(695)	VGGLIGLRIIFAVLSIVNRVQGYSPFSQTLTPSPRGFDRLGGIEEGG			
TV2.12-5/1	(680)	VGGLIGLRIIFAVLSIVNRVQGYSPFSQTLTPSPRGFDRLGGIEEGG			
Consensus	(701)	VGGLIGLRIIFAVLSIVNRVQGYSPFSQTLTPSPRGFDRLGGIEEGG			

FIGURE 105B

		751	800
SF162	(725)	ERDRDRSSP YHQLL IN DDLS SL AK ST ER ED LL LA AI IV ELL AR-	
TV1.8_2	(743)	EQDRDRSIR VS G F LS AW TH LN CL SY TH ED PI LI AV AV ELL GH S	
TV1.8_5	(745)	EQDRDRSIR VS G F LS AW TH LN CL SY TH ED PI LI AV AV ELL GH S	
TV2.12-5/1	(730)	EQDSRSIR VS G F LS AW TH LN CL SY TH ED PI LI AV AV ELL GH S	
Consensus	(751)	EQDRDRSIR VS G F LS AW TH LN CL SY TH ED PI LI AV AV ELL GH S	850
		801	
SF162	(774)	-----R WEAL K Y W N L Q Y N I Q SL KN SA SL F PA IR FA W ET Y RI E	
TV1.8_2	(793)	SLRGLO R WEIL K YL GS LV Q Y W GLE L KK SA IS LD TI AI VA EG TD RI E	
TV1.8_5	(795)	SLRGLO R WEIL K YL GS LV Q Y W GLE L KK SA IS LD TI AI VA EG TD RI E	
TV2.12-5/1	(780)	SLRGLO R WEIL K YL GS LV Q Y W GLE L KK SA IS LD TI AI VA EG TD RI E	
Consensus	(801)	SLRGLO R WEIL K YL GS LV Q Y W GLE L KK SA IS LD TI AI VA EG TD RI E	851
		851	876
SF162	(818)	VAQRIGRA FL H I PP RI Q GF E AA LL-	
TV1.8_2	(843)	LVQRICRAILNIP RR I R Q GF E AA LL-	
TV1.8_5	(845)	LVQRICRAILNIP RR I R Q GF E AA LL-	
TV2.12-5/1	(830)	FIONLCRGIRN V PR RI Q GF E AA LLQ-	
Consensus	(851)	LVQRICRAILNIP RR I R Q GF E AA LL	

FIGURE 105C